SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gatanaga, T.
          Granger, G.A.

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
          Factor Receptor Releasing Enzyme Activity

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:
   (A) ADDRESSEE: MORRISON & FOERSTER
   (B) STREET: 755 PAGE MILL ROAD
   (C) CITY: Palo Alto
   (D) STATE: CA
   (E) COUNTRY: USA
   (F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: Diskette
   (B) COMPUTER: IBM Compatible
   (C) OPERATING SYSTEM: Windows
   (D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:
   (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
   (A) APPLICATION NUMBER: USSN 09/081,385
   (B) FILING DATE: 014-NOV-1998

(viii) ATTORNEY/AGENT INFORMATION:
   (A) NAME:
   (B) REGISTRATION NUMBER:
   (C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(ix) TELECOMMUNICATION INFORMATION:
   (A) TELEPHONE: 650-813-5600
   (B) TELEFAX: 650-494-0792
   (C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 4047 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCCAGGCTGG GGGCCGCCAG CTCCGGGAAG GCAGTCCTGG CCTGCGGATG GGGCCGCGCG   180
TGGGGCCCGG CGGGGCGGCC TCGGGAGGCG TCCAGGCTGC GGGAGCGGGA GGAGCGGCCG   240
TGCGGGCGCC AGCGCCGTGG GTGGAGGTCG CCGTCCCTCC TGAGGGGCAG CCAGTGCGTT   300
TGGGACCCGG GAGCAGAGCC CGCGCCTCCC CAGCGGCCTC CCCGGGGGTC TCACCGGGTC   360
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CTCAGGCGTC GGAGGAGCCC CCAGAAGGAC CTCGCGCCTT CCCGCCGGGC TCCGACCGCC   480
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GCACGACCCA GAGGCCAGCA GCAGAGGACG GGGCCGGGGC CGGGAGAGGG CGGGGAGGGC   600
GCTCCTGGGA GGTCAAGGCC AGGGCTAGAC TTTCAGGGTC ATGGCCTGGC CCCTCATCCC   660
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ATTTTCAGGA GTTTCAGGTG GAGACAAAGG CCAGGCCCAG GTGAAAATGT GGCAGTGACA    960
GAGTATGGGG TGAGAACCAC GGAGAGAGGA AGTCCCCGAG GCGGATGATG GGACAGAGAG   1020
CGGGGACCAG AATTTTTTAA AACGCATCTG AGATGCGTTT GGCAGACTCA TAGTTGTTTT   1080
CCTTTCACGG AGAAAGTGTG GGCAGAAGCC AGCTCTAAAG CCCAGGCTGC CCAGCCTGCA   1140
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GAGGTGATGA CTGCCTTCCA GGGGCCTGGC TGGCTGACAC TTTGCATGGC TCCTGGAGAA   1440
GAGGGATTGA GTGGAGTCCA CGGGTCATGG CCACGTCCTG GGTGCTGCCT CTGAGGCAGG   1500
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CATGGGGTCT CTCCTTCAGG AGGTCTGGGT GGGGCCGGAG ACTGTACCCC ACAAAGGGTC   1680
CCAGGTGAGG CGGATGTGGC CTGGCGCTGT GTGGCTCTGG ACCTAGTCCT TGGGCTTGGG   1740
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GTGGGGACAT TACATCTTCC TAGCTTGGAA CACACAGGCA GCCAGGGTTG TTATCCACAT   1860
TCCTCCTCCA TGTTCTTCTC TTGAGAACTT TTACCAGGTA TGTCAGGAGC TGGGCTCCAC   1920
CAGGGAGACT CAAGTGGAAA GCCCTCATCC TTGTCCTCCA GGAGACAGGA AAACCTATGG   1980
TTACAATTCC AGGGACAAGA GCGATGCATG TGAGGTGTGG CAAATCTCAC TGTTCAACTG   2040
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CAACTGAAGT GTTCTGTTGT AAAACAGGCA CTTGATTTGC TGGAAGGAAT GCTGTTTGTT   2400
CTTGCTGCGA CAAACATTGA GCAGCATTTA GTGGGCGGTT TATATCTTGT GGAGTAATGG   2460
GTGTTTTTGA AGTCTGTCCT GGGTACTGCA CATTAAAAGG AATATCATTT TCTGAAACAT   2520
TGCTATTTTC CACACCAGAA ATCATATCCT CTTGCTGGTC CATGTCTGAA GACCTTACAC   2580
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TTTGTTTTCT TTCTGGAGAA TCTAGCAAGA TATCTGGTGG AACATCTCGA GGTGATGAAC   2760
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TTGTTGAAGA ATCTCCATCG TCACTACTTA GCCTGTGCAC CATGTGTAGG TAGTCCTCAC   2940
TTGAACCATG TCTAGGATTA TCAGCATGAT GATTAGCTGA ATTGCCAGAC AACGGACCAG   3000
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AGCTGTCATT ACTTCCCATT TCCCAAACAC TGGGCGAATC GGCGTCTGAA TCCAAGGGGA   3780
GGCCGAGGCC GCTGTGGCGA GAGACTATAA TCCGGGCCGG GAGGGGGGGC GGCTACGGCT   3840
CCTCTTCCGT CTCCTCAGTG CGGGGAACAT GTAGAGCCGG GGGGAGACCA GCCGAGAAGA   3900
CAAATCGTTG CTTCTTCTTC CTCCTCCTCC TCCTTCTCCC ACATAGAAAC ACTCACAAAC   3960
ACCCGACCAC GGGCCCGAGC TACCGGGGGG GCATCGCCGC GGGCCCGGGA ACCAATTCTC   4020
CTGTCGGCGG GGGCGTCCTT TGGATCC                                       4047
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    (2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 739 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GGATCCAAAG GTCAAACTCC CCACCTGGCA CTGTCCCCGG AGCGGGTCGC GCCCGGCCGG     60
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ACCGGGTCAG TGAAAAAACG ATCAGAGTAG TGGTATTTCA CCGGCGGCCC GCAGGGCCGG    180
CGGACCCCGC CCCGGGCCCC TCGCGGGGAC ACCGGGGGGG CGCCGGGGGC CTCCCACTTA    240
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TTCTACACCT CTCATGTCTC TTCACCGTGC CAGACTAGAG TCAAGCTCAA CAGGGTCTTC    300
TTTCCCCGCT GATTCCGCCA AGCCCGTTCC CTTGGCTGTG GTTTCGCTGG ATAGTAGGTA    360
GGGACAGTGG GAATCTCGTT CATCCATTCA TGCGCGTCAC TAATTAGATG ACGAGGCATT    420
TGGCTACCTT AAGAGAGTCA TAGTTACTCC CGCCGTTTAC CCGCGCTTCA TTGAATTTCT    480
TCACTTTGAC ATTCAGAGCA CTGGGCAGAA ATCACATCGC GTCAACACCC GCCGCGGGCC    540
TTCGCGATGC TTTGTTTTAA TTAAACAGTC GGATTCCCCT GGTCCGCACC AGTTCTAAGT    600
CGGCTGCTAG GCGCCGGCCG AAGCGAGGCG CCGCGCGGAA CCGCGGCCCC CGGGGCGGAC    660
CCGCGGGGGG GACCGGGCCG CGGCCCCTCC GCCGCCTGCC GCCGCCGCCG CCGCCGCGCG    720
CCGAAGAAGA AGGGGGAAA                                                 739
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        (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 233 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCCCCGCCGC CGCCCCCACG CGGCGCTCCC CCGGGGAGGG GGGAGGACGG GGAGCGGGGG    180
AGAGAGAGAG AGAGAGAGGG CGCGGGGTGG CTCGTGCCGA ATTCAAAAAG CTT           233
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        (2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2998 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CCGTCCAGCG ACAGCTTGGC GTGCTGGGCG CTCACGGGGT CCGCATACTG CAGCAGGGCC    180
TGGAACTGGT TGTTCTTGGT GAAGGTGATG ATCTTCAACA CTGTGCCGAA CTTGGAGAAA    240
ATCTGGTGCA GCACATCCAG GGTCACAGGG TAGAAGAGGT TCTCCACGAT GATCCTGAGC    300
ACGGGGCTCT GCCCGGCCAT CGCCATCCCT GCATCCACGG CCGCCGCCGA GGCAGCCAAG    360
GCCAGGTTCC CCGACTGGAC CGAGTTCACC GCCTGCAGGG CCGCCTGGGC CGCGCCTGG     420
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CCGCGCAGCA CAGGGGTCAC CGAGGTGTAG TAGTTCACCA TGGTATTGGC AGCCTCCTCC    540
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CCAAAGGGCA GCCCCAGGGA GATGACTTCC CCCTCCGTGA CGTCGATGGG GAGCTTCCGG    660
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GCTAGAGCTG CAGATTGAGT TGCTGCGTGA GACGAAGCGC AAGTATGAGA GTGTCCTGCA    960
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TGCAGAGACA CAGAAACTAC TATGCAAGAA TGGGGAAACG CTGCTAGGAG CCGTGAACTT   1140
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GAAACAGTAT GAGGCTGCCA GGCTGGAATA TGATGCCTAC CGAACAGACT TAGAGGAGCT   1260
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CCAGGCCCAT CGGGACAAGT ATGAGAAGCT GCGGGGAGAT GTGGCCATCA AGCTCAAGTT   1380
CCTGGAAGAA AACAAGATCA AGGTGATGCA CAAGCAGCTG CTGCTCTTCC ACAATGCTGT   1440
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CAAGCTGCGG CCTCCAGGAG CTGAGAAACC CTCCTGGCTA GAGGAGCAGT GAGCTGCTCC   1560
CAGCCCAACT TGGCTATCAA GAAAGACATT GGGAAGGGCA GCCCCAGGGT GTGGGAGATT   1620
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CTGACACCAG TTTTGCCCAC ATTGCTATGG TGGGAAGAGG GCCTGGAGGC CCAGAAGTTG   1740
CTGCCCTGTC TATCTTCCTG GCCACAGGGC TTCATTCCCA GATCTTTTCC TTCCACTTCA   1800
CAGCCAACGG CTATGACAAA ACCACTCCCT GGCCAATGGC ATCACTCTTC AGGCTGGGGT   1860
GTGCTCCCTG ACCAATGACA GAGCCTGAAA ATGCCCTGTC AGCCAATGGC AGCTCTTCTC   1920
GGACTCCCCT GGGCCAATGA TGTTGCGTCT AATACCCTTT GTCTCTCCTC TATGCGTGCC   1980
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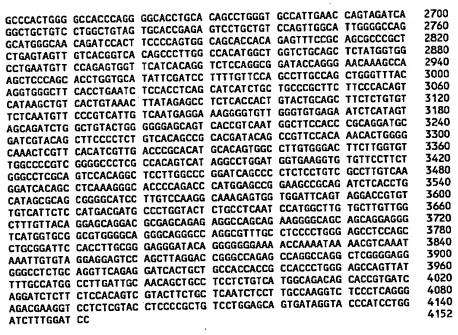
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TAGTTTTTCC CCTAAAAAAT TCAATGGCAT TCTTTCTTAT AAATTACATT CTCTGATTTT   2220
CTTGTCAGCC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTTGCTCGCA GTTTGCTCCA   2280
TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAT TGAGCTGATC CTTCTGGAGA   2340
AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCACA CATCCTGAAC   2400
TCCCCAGTCT GGTGTGAGGG GAGGACAGCT GATAACTGGA TATGCAGTGT TCCCAGACAT   2460
CACTGGTCCC AAACCATTAC TTCTGCCTGC CACTGCCACA AATACAGTAG GAATGCCATC   2520
CCCTTCATAC TCAGCTTTAA TCCTCAGAGT TTCATCTGGT CCTTTATGCG CAGATGTTAC   2580
TCGAAGTTCA CATGGAATGC CAAAATTTCC ACAGGCCTTC TTGATTTTTT CACAGTGACC   2640
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CAACTCTACT CTCTCTGCAA CCCACTCAAA GTTTTTCTTT ACCATTTGGA GCCCTTCAGG   2760
AGTTACTTCT TTGAGGTCCC GATAAGACTG TTTGTCTTTC TGTTGGCTTC GATCTCCTGA   2820
TGGCCAGAGT CTCCAGGAAT CATTGTCAAT AACATCAGCA AGAACAATTT CTTTGGTGGT   2880
TACATCAACA CCAAATTCAA TCTTCATATC AACCAGTGTA CAATTCTGGG GCAACCAGGA   2940
TTTCTCCAGT ATTTCAAATA TAGCCTGTGT AGCATCTCGT GCCGAATTCA AAAAGCTT    2998
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(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 4152 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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TATGTACACC CGGGGCCCCC ACGTCCCCTC CCGTCCCCGC AGCCTGGCCA CACCAGGTCA    240
CGGAGGAGGG GCCGGGGCTG CAGGACCTCA GGACTGCAAG GGCAGGAAGG GAAACAGGAC    300
AAGAAAGGAA GGAAGTTGGA AAGGAGGGAG AAATGGGGTC CCCAGACTGA AATGGAAATG    360
AGGTGGGGCG ATCATAAGAG AAGCAGGGAC GATGGTCCAG CTGAGGGAGC CCTGCAGAGG    420
GGGAAAAGCT TCCCATGGAC AGGAGAGAGA AGGGAAGGGG AGAGGAGAGG GTTTCCTTCA    480
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CTTTCCAACC CAGCCAGCCC CAGTGCAAGG GGCACACCAG GAGCATGACA GCCCAGAAGT    660
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TCCTTCTCCC ATGTCTGGAG TGTCTGTTTC ACCAGGGCAG AATTCCCCCT CTGCGTGGGG    840
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TGGGGGAATC GGCCACCTCC GAGTCACTGC TGTCCTCATC CTCCTGCTGG CCCCCAACAG    960
CCCCCGTCAC ACAGGACTGC CGATTCTGGT AGGACTCCAT GGGGGTTCACA ATGATGGTGA   1020
GAGCTGAGTC ATCCCAGAAG AGGTCTGGGT CCTTGGGGTC ACTGGAGGCC CCTGGAGGCC   1080
CGCCGGCCCC TGAGACGCGG CGGTGAAGGG AATGGATGCG CACCAGGCCC AGGACGACCA   1140
TGAGCACCAG GAAGCCCACG CACACCACAA TGATGAGGGT TGCGGCGCTG GGTATCATGG   1200
AGTTTCTGTG GGAGCTGGCT AGGCTGTGTC CAGCCATCTC AGGCGGGGGC TGGTGACCAC   1260
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CCTGAATGTT CCAGAGTGGT TCATCACAGG TCTCCAGGCG GATACCAGGG AACAAAGCCA    2940
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GGATCACAGC CTCAAAGGGC ACCCCAGACC CATGGAGCCG GAAGCCGCAG ATCTCACCTG    3540
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CTTTGTTACA GGAGCAGGAC GCGAGCAGAG AGGCCAGCAG AAGGGGCAGC AGCAGGAGGG    3720
TCATGGTGCG GCGTGGGGCA GGGCAGGGCC AGGCGTTTGC CTCCCCTGGG AGCCTCCAGC    3780
CTGCGGATTC CACCTTGCGG GAGGGATACA GGGGGGGAAA ACCAAAATAA AACGTCAAAT    3840
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        (2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 3117 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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AGAACAAGCG GAAGCGTTGC CTCTTTGGGG GCCAGGAACC AGCTCCCAAG GAGCAGCCCC     120
CTCCCCTGCA GCCCCCCCAG CAGTCCATCA GAGTGAAGGA GGAGCAGTAC CTCGGGCACG     180
AGGGTCCAGG AGGGGCAGTC TCCACCTCTC AGCCTGTGGA ACTGCCCCCT CCTAGCAGCC     240
TGGCCCTGCT GAACTCTGTG GTGTATGGGC CTGAGCGGAC CTCAGCAGCC ATGCTGTCCC     300
AGCAGGTGGC CTCAGTAAAG TGGCCCAACT CTGTGATGGC TCCAGGGCGG GGCCCGGAGC     360
GTGGAGGAGG TGGGGGTGTC AGTGACAGCA GCTGGCAGCA GCAGCCAGGC CAGCCTCCAC     420
CCCATTCAAC ATGGAACTGC CACAGTCTGT CCCTCTACAG TGCAACCAAG GGGAGCCCGC     480
ATCCTGGAGT GGGAGTCCCG ACTTACTATA ACCACCCTGA GGCACTGAAG CGGGAGAAAG     540
CGGGGGGCCC ACAGCTGGAC CGCTATGTGC GACCAATGAT GCCACAGAAG GTGCAGCTGG     600
AGGTAGGGCG GCCCCAGGCA CCCCTGAATT CTTTCCACGC AGCCAAGAAA CCCCCAAACC     660
AGTCACTGCC CCTGCAACCC TTCCAGCTGG CATTCGGCCA CCAGGTGAAC CGGCAGGTCT     720
TCCGGCAGGG CCCACCGCCC CCAAACCCGG TGGCTGCCTT CCCTCCACAG AAGCAGCAGC     780
AGCAGCAGCA ACCACAGCAG CAGCAGCAGC AGCAGCAGGC AGCCCTACCC CAGATGCCGC     840
TCTTTGAGAA CTTCTATTCC ATGCCACAGC AACCCTCGCA GCAACCCCAG GACTTTGGCC     900.
TGCAGCCAGC TGGGCCACTG GGACAGTCCC ACCTGGCTCA CCACAGCATG GCACCCTACC     960
CCTTCCCCCC CAACCCAGAT ATGAACCCAG AACTGCGCAA GGCCCTTCTG CAGGACTCAG    1020
CCCCGCAGCC AGCGCTACCT CAGGTCCAGA TCCCCTTCCC CCGCCGCTCC CGCCGCCTCT    1080
CTAAGGAGGG TATCCTGCCT CCCAGCGCCC TGGATGGGGC TGGCACCCAG CCTGGGCAGG    1140
AGGCCACTGG CAACCTGTTC CTACATCACT GGCCCCTGCA GCAGCCGCCA CCTGGCTCCC    1200
TGGGGCAGCC CCATCCTGAA GCTCTGGGAT TCCCGCTGGA GCTGAGGGAG TCGCAGCTAC    1260
TGCCTGATGG GGAGAGACTA GCACCCAATG GCCGGGAGCG AGAGGCTCCT GCCATGGGCA    1320
GCGAGGAGGG CATGAGGGCA GTGAGCACAG GGGACTGTGG GCAGGTGTGA CGGGGCGGAG    1380
TGATCCAGAG CACGCGACGG AGGCGCCGGG CATCCCAGGA GGCCAATTTG CTGACCCTGG    1440
CCCAGAAGGC TGTGGGAGCTG GCCTCACTGC AGAATGCAAA GGATGGCAGT GGTTCTGAAG    1500
AGAAGCGGAA AAGTGTATTG GCCTCAACTA CCAAGTGTGG GGTGGAGTTT TCTGAGCCTT    1560
CCTTAGCCAC CAAGCGAGCA CGAGAAGACA GTGGGATGGT ACCCCTCATC ATCCCAGTGT    1620
CTGTGCCTGT GCGAACTGTG GACCCAACTG AGGCAGCCCA GGCTGGAGGT CTTGATGAGG    1680
ACGGGAAGGG TCTTGAACAG AACCCTGCTG AGCACAAGCC ATCAGTCATC GTCACCCGCA    1740
GGCGGTCCAC CCGAATCCCC GGGACAGATG CTCAAGCTCA GGCGGAGGAC ATGAATGTCA    1800
AGTTGGAGGG GGAGCCTTCC GTGCGGAAAC CAAAGCAGCG GCCCAGGCCC GAGCCCCTCA    1860
TCATCCCCAC CAAGGCGGGC ACTTTCATCG CCCCTCCCGT CTACTCCAAC ATCACCCCAT    1920
ACCAGAGCCA CCTGCGCTCT CCCGTGCGCC TAGCTGACCA CCCCTCTGAG CGGAGCTTTG    1980
AGCTACCTCC CTACACGCCG CCCCCCATCC TCAGCCCTGT GCGGGAAGGC TCTGGCCTCT    2040
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ACTTCAATGC CATCATATCA ACCAGCACCA TCCCTGCCCC TCCTCCCATC ACGCCTAAGA    2100
GTGCCCATCG CACGCTGCTC CGGACTAACA GTGCTGAAGT AACCCCGCCT GTCCTCTCTG    2160
TGATGGGGGA GGCCACCCCA GTGAGCATCG AGCCACGGAT CAACGTGGGC TCCCGGTTCC    2220
AGGCAGAAAT CCCCTTGATG AGGGACCGTG CCCTGGCAGC TGCAGATCCC CACAAGGCTG    2280
ACTTGGTGTG GCAGCCATGG GAGGACCTAG AGAGCAGCCG GGAGAAGCAG AGGCAAGTGG    2340
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TGGCCCTGCA CTGTCTGCAC GAATCCAGAG GAGACATCCT GGAAACGCTG AATAAGCTGC    2460
TGCTGAAGAA GCCCCTGCGG CCCCACAACC ATCCGCTGGC AACTTATCAC TACACAGGCT    2520
CTGACCAGTG GAAGATGGCC GAGAGGAAGC TGTTCAACAA AGGCATTGCC ATCTACAAGA    2580
AGGATTTCTT CCTGGTGCAG AAGCTGATCC AGACCAAGAC CGTGGCCCAG TGCGTGGAGT    2640
TCTACTACAC CTACAAGAAG CAGGTGAAAA TCGGCCGCAA TGGGACTCTA ACCTTTGGGG    2700
ATGTGGATAC GAGCGATGAG AAGTCGGCCC AGGAAGAGGT TGAAGTGGAT ATTAAGACTT    2760
CCCAAAAGTT CCCAAGGGTG CCTCTTCCCA GAAGAGAGTC CCCAAGTGAA GAGAGGCTGG    2820
AGCCCAAGAG GGAGGTGAAG GAGCCCAGGA AGGAGGGGGA GGAGGAGGTG CCAGAGATCC    2880
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CCACGCAGAC ACTACAGGCC AATGAGTCGG CCAGTGACAT CCTCATCCTC CGGAGCCACG    3000
AGTCCAACGC CCCTGGGTCT GCCGGTGGCC AGGCCTCGGA GAAGCCAAGG GAAGGGACAG    3060
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TTAATCCGCT AAACAGTTCG CAAGGATATA ACGTCTCTGG CATTGGGAAG ATTTTTATGT     180
TTAATGTCTG CGGCACAATG CCTGTCTGTG GGACCATCCT GGGAAAACCT GCTTCTGGCT     240
GTGAGGCAGA AACCCAAACT GAAGAGCTCA AGAATTGGAA GCCAGCAAGG CCAGTCGGAA     300
TTGAGAAAAG CCTCCAGCTG TCCACAGAGG GCTTCATCAC TCTGACCTAC AAAGGGCCTC     360
TCTCTGCCAA AGGTACCGCT GATGCTTTTA TCGTCCGCTT TGTTTGCAAT GATGATGTTT     420
ACTCAGGGCC CCTCAAATTC CTGCATCAAG ATATCGACTC TGGGCAAGGG ATCCGAAACA     480
CTTACTTTGA GTTTGAAACC GCGTTGGCCT GTGTTCCTTC TCCAGTGGAC TGCCAAGTCA     540
CCGACCTGGC TGGAAATGAG TACGACCTGA CTGGCCTAAG CACAGTCAGG AAACCTTGGA     600
CGGCTGTTGA CACCTCTGTC GATGGGAGAA AGAGGACTTT CTATTTGAGC GTTTGCAATC     660
CTCTCCCTTA CATTCCTGGA TGCCAGGGCA GCGCAGTGGG GTCTTGCTTA GTGTCAGAAG     720
GCAATAGCTG GAATCTGGGT GTGGTGCAGA TGAGTCCCCA AGCCGCGGCG AATGGATCTT     780
TGAGCATCAT GTATGTCAAC GGTGACAAGT GTGGGAACCA GCGCTTCTCC ACCAGGATCA     840
CGTTTGAGTG TGCTCAGATA TCGGGCTCAC CAGCATTTCA GCTTCAGGAT GGTTGTGAGT     900
ACGTGTTTAT CTGGAGAACT GTGGAAGCCT GTCCCGTTGT CAGAGTGGAA GGGGACAACT     960
GTGAGGTGAA AGACCCAAGG CATGGCAACT TGTATGACCT GAAGCCCCTG GGCCTCAACG    1020
ACACCATCGT GAGCGCTGGC GAATACACTT ATTACTTCCG GGTCTGTGGG AAGCTTTCCT    1080
CAGACGTCTG CCCCACAAGT GACAAGTCCA AGGTGGTCTC CTCATGTCAG GAAAAGCGGG    1140
AACCGCAGGG ATTTCACAAA GTGGCAGGTC TCCTGACTCA GAAGCTAACT TATGAAAATG    1200
GCTTGTTAAA AATGAACTTC ACGGGGGGGG ACACTTGCCA TAAGGTTTAT CAGCGCTCCA    1260
CAGCCATCTT CTTCTACTGT GACCGCGGCA CCCAGCGGCC AGTATTTCTA AAGGAGACTT    1320
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GAGATGGCAT AATTGTCCTG AAATACGTTG ATGGCGACTT ATGTCCAGAT GGGATTCGGA    1680
AAAAGTCAAC CACCATCCGA TTCACCTGCA GCGAGAGCCA AGTGAACTCC AGGCCCATGT    1740
TCATCAGCGC CGTGGAGGAC TGTGAGTACA CCTTTGCCTG GGCCACAGCC ACAGCCTGTC    1800
CCATGAAGAG CAACGAGCAT GATGACTGCC AGGTCACCAA CCCAAGCACA GGACACCTGT    1860
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TCCTGCAGCT GGTGTACAAG GATGGGTCCC CTTGTCCCTC CAAATCCGGC CTGAGCTATA    2100
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TCTCCCTGGA CAAGCAGACA TGCACTCTCT TCTTCTCCTG GCACACGCCG CTGGCCTGCG    2220
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ACCCTGATTT CTACATCAAT ATTTGTCAGC CACTAAATCC CATGCACGGA GTGCCCTGTC    2400
CTGCCGGAGC CGCTGTGTGC AAAGTTCCTA TTGATGGTCC CCCCATAGAT ATCGGCCGGG    2460
TAGCAGGACC ACCAATACTC AATCCAATAG CAAATGAGAT TTACTTGAAT TTTGAAAGCA    2520
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GTACTCCTTG CCAGGAATTC AGTTGTAAAT AAAATTGAAC CTGCTCAACA GCTGAGGGAG    2580
ACTAGAAATG ATGGGTCCAT ATCCTGGTGC ATTGTCATAC AATTCAAACA ATGGGTGCAGC   2640
TACCAGCTTG TAATTTTTAG GGACTGCAAA CAAGGCTTTT TCTTGAAGCT GAACCAGAAA    2700
CAACTTCTTA TGTTCCTTAG GCTTTGTAAT ATGTGCAGGA ATATATGGAT ACTGAGGAGG    2760
TTCAAAATTT GGTCTCCACC AGTTACCAAT GCAATCGTCA ATGACCCAGT CTTGCAAAAC    2820
TCCATCCTGA CGACCCAGTA TCTCTGTCAT TAAGCGTTTT AGTCCTTCAA CTTCATCTTC    2880
TCCTGGGTTA AGTTCACCAC CAGGTAGTTT GAAGAAAGTT GTTCCCAGCT GCAGCAGTAA    2940
CACATGGGGT AGCCGGTGCT CATGTACAAT CAGAACCCCT TCTACAGTCC TCCTCATTCC    3000
AATTTTATCA AATTCTTCCC TCATGCGCTG AAATCTGGCT GCAACAGAGC TGTCCTTCTC    3060
GTAGAGGGGC TCTTTTGTAC CAAAAGTATA ATTGGTAAGA GGGTACAGGT TGATGGTGCG    3120
CTCCAGGGTG AGGGGCTTCG TCTGCTGGAT GTACTTGTTG CCGAACTGAG TGACCCCCCG    3180
GGGCCAGCCG GTCTGCGAGC GATTGGGCGG TACCACAGAC ATGCTGGCGA GCTCCGGCGC    3240
TGACGGCGAG CAGAAAGTGG CAGGCAGGGT AGACTTTCCC CGTGCGGGAA GCCTCGTGCC    3300
GAATTC                                                                3306
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        (2) INFORMATION FOR SEQ ID NO:8:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 4218 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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GATTGGTGGT TGCCAGGGAC AAGGGCGGTG GGAGGAGAAA ATGGAGAGTA ACGGGACTTT     180
ACTTTTGGAG TGATGAGAAT GTTTTGGAGC TAGATAGAAG TGGTGGTTGT ACACCATTGT     240
GGATGTACTA CCACTTAATT GTTCACTTAA AAAGTTAATT TATGTGAATT GCATCTTAAT     300
TAAAAACAAG GATAACATTC CAACTCCTGG ACATTATCCT TCCTTTCCAT TTGATGTCAG     360
GCCCGTGTTA GAATTCTCAT CCGGTTTGGT CACTGCACTT AAGATGTGGA GAAATTAGGA     420
CGCACAGTTA AGAGGAAGGA TAACACTGAT TAAGGTAGTG CTTTTCTAGG TTTCCCCTAA     480
ACAATTTAAC AGATGGATAG TGGCACCACT TACGAGATGG AAAAACCAGC GGAAGGAAGA     540
TTTGGGGGAG AAGTTAAGTT TGTCTTGGGC CTGTGTTTTG CAACCTGAGT GTAAAAGACA     600
TATGTTAAGT CTTCAGTGGC GAAACACTAA AACTAGAAAT GGATCAGAAT TTTATCTTTG     660
GATGTGACTT CTCAAGGATG GTCTTGTCAC TTCAGTGCCT GGTCAAATGA CAAGATGGGC     720
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TAGAACAATC CTAGTTCATG CCTATTGTCC CTCATGTAAT TAATATCACT CTCAAAATGT     840
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CTAGATTACT GCCAGTTCCT CATGGACCAG GGGCGCGTCA CACACACCCG CCGCACCTTC    1260
GACCGTGCCC TCCGGGCACT GCCCATCACG CAGCACTCTC GAATTTGGCC CCTGTATCTG    1320
CGCTTCCTGC GCTCACACCC ACTGCCTGAG ACAGCTGTGC GAGGCTATCG GCGCTTCCTC    1380
AAGCTGAGTC CTGAGAGTGC AGAGGAGTAC ATTGAGTACC TCAAGTCAAG TGACCGGCTG    1440
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AAGGTACAGT CCCTCAATGT GGACGCCATC ATCCGCGGGG GCCTCACCCG CTTCACCGAC    1620.
CAGCTGGGCA AGCTCTGGTG TTCTCTCGCC GACTACTACA TCCGCAGCGG CCATTTCGAG    1680
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CAGGTGTTTG ACAGCTACGC CCAGTTCGAG GAGAGCATGA TCGCTGCAAA GATGGAGACC    1800
GCCTCGGAGC TGGGGCGCGA GGAGGAGGAT GATGTGGACC TGGAGCTGCG CCTGGCCCGC    1860
TTCGAGCAGC TCATCAGCCG GCGGCCCCTG CTCCTCAACA GCGTCTTGCT GCGCCAAAAC    1920
CCACACCACG TGCACGAGTG GCACAAGCGT GTCGCCCTGC ACCAGGGCCG CCCCCGGGAG    1980
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TCCGACATCT GGAGCACCTA CCTGACCAAA TTCATTGCCC GCTATGGGGG CCGCAAGCTG    2580
GAGCGGGCAC GGGACCTGTT TGAACAGGCT CTGGACGGCT GCCCCCCAAA ATATGCCAAG    2640
ACCTTGTACC TGCTGTACGC ACAGCTGGAG GAGGAGTGGG GCCTGGCCCG GCATGCCATG    2700
GCCGTGTACG AGCGTGCCAC CAGGGCCGTG GAGCCCGCCC AGCAGTATGA CATGTTCAAC    2760
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ATGGAGTGCA AGCTCGGGGA GATTGACCGC GCCCGGGCCA TCTACAGCTT CTGCTCCCAG    2940
ATCTGTGACC CCCGGACGAC CGGCGCGTTC TGGCAGACGT GGAAGGACTT TGAGGTCCGG    3000
CATGGCAATG AGGACACCAT CAAGGAAATG CTGCGTATCC GGCGCAGCGT GCAGGCCACG    3060
TACAACACGC AGGTCAACTT CATGGCCTCG CAGATGCTCA AGGTCTCGGG CAGTGCCACG    3120
GGCACCGTGT CTGACCTGGC CCCTGGGCAG AGTGGCATGG ACGACATGAA GCTGCTGGAA    3180
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GTCAACCCCG AGGAGATCCA GCTGGGCGAG GACGAGGACG AGGACGAGAT GGACCTGGAG    3360
CCCAACGAGG TTCGGCTGGA GCAGCAGAGC GTGCCAGCCG CAGTGTTTGG GAGCCTGAAG    3420
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CCAGGGCATG GGGTGCTGTG AGGGCAGCAT GCTAGGTGTG ACCGTGCTCC TGGCCTCCAG    3720
GCCCGTGTCC CTCTGTCCTC TAGCCCACTA AGGCCCTGGC CCATTTGTGC TAAACAGGCA    3780
GTCGGACCTA GAAAGAGCAG ACAATCTCTC TGGGTCACCA GTCTGGCTAG GAGCTGGTCT    3840
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CCTGCCTGCT TTCGTGGGTT CAGAGTAGCT GAGGCTTGTC TGAGAGGAGT TGGAGTGCTG    4020
GTTTTCACCC TGGTTGGTGT GCTTTGCTTT GAGGGCACTT AGAAAGCCCA GCCCAGCCCT    4080
TGCTCCTGCC CTGCACACAG CGGAGCGACT TTTCTAGGTA TGCTCTTGAT TTCTGCAGAA    4140
GCAGCAGGTG GCATGGAGCC AAGAGGAAGT GTGACTGAAA CTGTCCACTC ATAGCCCGGC    4200
TGCCGTATTG AGAGGGCT                                                  4218
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          (2) INFORMATION FOR SEQ ID NO:9:

              (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 1187 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

              (ii) MOLECULE TYPE: Genomic DNA

              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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CAGTGTCTGA GGGGACTGAC TCTGGCATCT CTGCCGAGGC TGCTGGAATC GACTGGGGCA     240
TCTTCCCGGA ATCAGATTCA AAGGATCCTG GAGGTGATGG GATAGACTGG GGAGACGATG     300
CTGTTGCTTT GCAGATCACA GTGCTGGAAG CAGGAACCCA GGCTCCAGAA GGTGTTGCCA     360
GGGGCCCAGA TGCCCTGACA CTGCTTGAAT ACACTGAGAC CCGGAATCAG TTCCTTGATG     420
AGCTCATGGA GCTTGAGATC TTCTTAGCCC AGAGAGCAGT GGAGTTGAGT GAGGAGGCAG     480
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TCCTCCAGCA AAAGCTGAAG CAGTCCCAGC TGCTGGCTTT GAAGAAAGAG CTGATGGTGC     720
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GGCGCCCTGT GAACCTGATG GGAACCTCTC TGTGACACCC TCCGTGTTCT TGCCTGCCCA     900
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          (2) INFORMATION FOR SEQ ID NO:10:

              (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 3306 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

              (ii) MOLECULE TYPE: Genomic DNA

              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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GTGACTTCAT CGACAACCTG GACAGACCTC CAGGTTCCTC CTACTTCCGC TATGCTGAGT   1860
CTTCCATGAA GAACAGCTTC GGCCTAAAGT ACCTTCATAA GTTCTTCAAT ATCCCATTTT   1920
TGCAGCTTCA GAGGGAGACG CTGTTGCGGC AGCTGGAGAC GAACCAGCTG GACATGGACG   1980
CCACGCTGGA GGAGCTGTCG GTGCAGCAGG AGACGGAGGA CCAGAACTAC GGCATCTTCC   2040
TGGAGATGAT GGAGGCTCGC AGCCGTGGCC ATGCGTCCCC ACTGGCGGCC AACGGGCAGA   2100
GCCCATCCCC GGGCTCCCAG TCACCAGTCC TGCCTGCACC CGCTGTGTCC ACGGGGAGCT   2160
CCAGCCCCGG CACACCCCAG CCCGCCCCAC AGCTGCCCCT CAATGCTGCC CCACCATCCT   2220
CTGTGCCCCC TGTACCACCC TCAGAGGCCC TGCCCCCACC TGCGTGCCCC TCAGCCCCCG   2280
CCCCACGGCG CAGCATCATC TCTAGGCTGT TTGGGACGTC ACCTGCCACC GAGGCAGCCC   2340
CTCCACCTCC AGAGCCAGTC CCGGCCGCAC AGGGCCCAGC AACGGTCCAG AGTGTGGAGG   2400
ACTTTGTTCC TGACGACCGC CTGGACCGCA GCTTCCTGGA AGACACAACC CCCGCCAGGG   2460
ACGAGAAGAA GGTGGGGGCC AAGGCTGCCC AGCAGGACAG TGACAGTGAT GGGGAGGCCC   2520
TGGGCGGCAA CCCGATGGTG GCAGGGTTCC AGGACGATGT GGACCTCGAA GACCAGCCAC   2580
GTGGGAGTCC CCCGCTGCCT GCAGGCCCCG TCCCCAGTCA AGACATCACT CTTTCGAGTG   2640
AGGAGGAAGC AGAAGTGGCA GCTCCCACAA AAGGCCCTGC CCCAGCTCCC CAGCAGTGCT   2700
CAGAGCCAGA GACCAAGTGG TCCTCCATAC CAGCTTCGAA GCCACGGAGG GGGACAGCTC   2760
CCACGAGGAC CGCAGCACCC CCCTGGCCAG GCGGTGTCTC TGTTCGCACA GGTCCGGAGA   2820
AGCGCAGCAG CACCAGGCCC CCTGCTGAGA TGGAGCCGGG GAAGGGTGAG CAGGCCTCCT   2880
CGTCGGAGAG TGACCCCGAG GGACCCATTG CTGCACAAAT GCTGTCCTTC GTCATGGGATG   2940
ACCCCGACTT TGAGAGCGAG GGATCAGACA CACAGCGCAG GGCGGATGAC TTTCCCGTGC   3000
GAGATGACCC CTCCGATGTG ACTGACGAGG ATGAGGGCCC TGCCGAGCCG CCCCCACCCC   3060
CCAAGCTCCC TCTCCCCGCC TTCAGACTGA AGAATGACTC GGACCTCTTC GGGCTGGGGC   3120
TGGAGGAGGC CGGACCCAAG GAGAGCAGTG AGGAAGGTAA GGAGGGCAAA ACCCCCTCTA   3180
AGGAGAAGAA AAAAAAAACA AAAAGCTTCT CGAGAGTACT TCTAGAGCGG CCGCGGGCCC   3240
ATCGATTTTC CACCCGGGTG GGGTACCAGG TAAGTGTACC CAATTCGCCC TATAGTGAGT   3300
CGTATT                                                            3306
```

        (2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

                                                                    20
    TGCGGGGCCA GAGTGGGCTG

        (2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid

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```
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG                                              20

              (2) INFORMATION FOR SEQ ID NO:13:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC                                              20

              (2) INFORMATION FOR SEQ ID NO:14:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTC GGTGCGGGAC                                              20

              (2) INFORMATION FOR SEQ ID NO:15:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG                                              20

              (2) INFORMATION FOR SEQ ID NO:16:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCCGT CTCCTCAGTG                                              20

              (2) INFORMATION FOR SEQ ID NO:17:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC                                              20
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC   20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCCTC CCTGTCACAG   20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG   20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCC AGAAATTCAG   20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC   20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAGGGAG   20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAACCTATG GTTACAATTC   20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAAGTG   20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC   20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC   20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC   20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCCTGAG   20

          (2) INFORMATION FOR SEQ ID NO:30:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC   20

          (2) INFORMATION FOR SEQ ID NO:31:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCACTGGGG ACTCCGGCAG   20

          (2) INFORMATION FOR SEQ ID NO:32:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTTCCC TGGGCACATG   20

          (2) INFORMATION FOR SEQ ID NO:33:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCCAG   20

          (2) INFORMATION FOR SEQ ID NO:34:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG   20

       (2) INFORMATION FOR SEQ ID NO:35:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC   20

       (2) INFORMATION FOR SEQ ID NO:36:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG   20

       (2) INFORMATION FOR SEQ ID NO:37:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG   20

       (2) INFORMATION FOR SEQ ID NO:38:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG   20

       (2) INFORMATION FOR SEQ ID NO:39:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCGAGAG   20

       (2) INFORMATION FOR SEQ ID NO:40:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC   20

            (2) INFORMATION FOR SEQ ID NO:41:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG   20

            (2) INFORMATION FOR SEQ ID NO:42:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTTGAAT TCGGCACGAG   20

            (2) INFORMATION FOR SEQ ID NO:43:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCTGGTCC GCACCAGTTC   20

            (2) INFORMATION FOR SEQ ID NO:44:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCGGCAG   20

            (2) INFORMATION FOR SEQ ID NO:45:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC   20

            (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC   **20**

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG   **20**

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC   **20**

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCGTTGT AGATGTTCTG   **20**

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG   **20**

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG   20

    (2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTCAGAT GCAACGCCAG   20

    (2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGGCACA CAGAGCAGAC   20

    (2) INFORMATION FOR SEQ ID NO:54:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG   20

    (2) INFORMATION FOR SEQ ID NO:55:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG   20

    (2) INFORMATION FOR SEQ ID NO:56:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACGCATA GAGGAGAGAC   20

    (2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC   20

            (2) INFORMATION FOR SEQ ID NO:58:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 20 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG   20

            (2) INFORMATION FOR SEQ ID NO:59:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 20 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCCACAT TGCTATGGTG   20

            (2) INFORMATION FOR SEQ ID NO:60:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 20 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG   20

            (2) INFORMATION FOR SEQ ID NO:61:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 20 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCTGGGCC AATGATGTTG   20

            (2) INFORMATION FOR SEQ ID NO:62:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 19 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCACC ATAGCAATG   19

(2) INFORMATION FOR SEQ ID NO:63:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG   20

       (2) INFORMATION FOR SEQ ID NO:64:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG   20

       (2) INFORMATION FOR SEQ ID NO:65:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG   20

       (2) INFORMATION FOR SEQ ID NO:66:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCACGAC   20

       (2) INFORMATION FOR SEQ ID NO:67:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG   20

       (2) INFORMATION FOR SEQ ID NO:68:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGGCGATC   20

        (2) INFORMATION FOR SEQ ID NO:69:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTGCCTTG GACAAGGATG   20

        (2) INFORMATION FOR SEQ ID NO:70:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG   20

        (2) INFORMATION FOR SEQ ID NO:71:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGGAAGCC ATTGACGGTG   20

        (2) INFORMATION FOR SEQ ID NO:72:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG   20

        (2) INFORMATION FOR SEQ ID NO:73:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG   20

        (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG   20

        (2) INFORMATION FOR SEQ ID NO:75:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG   20

        (2) INFORMATION FOR SEQ ID NO:76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC   20

        (2) INFORMATION FOR SEQ ID NO:77:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCAC   20

        (2) INFORMATION FOR SEQ ID NO:78:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTC CCTGATCTTC   20

        (2) INFORMATION FOR SEQ ID NO:79:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCATC   20

       (2) INFORMATION FOR SEQ ID NO:80:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG   20

       (2) INFORMATION FOR SEQ ID NO:81:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC   20

       (2) INFORMATION FOR SEQ ID NO:82:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG   20

       (2) INFORMATION FOR SEQ ID NO:83:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG   20.

       (2) INFORMATION FOR SEQ ID NO:84:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid ·
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG   20

       (2) INFORMATION FOR SEQ ID NO:85:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC   20

            (2) INFORMATION FOR SEQ ID NO:86:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTAG CTCAAAGCTC   20

            (2) INFORMATION FOR SEQ ID NO:87:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCGCACAG   20

            (2) INFORMATION FOR SEQ ID NO:88:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG   20

            (2) INFORMATION FOR SEQ ID NO:89:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAAGAC   20

            (2) INFORMATION FOR SEQ ID NO:90:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 20 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC   20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG   20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG   20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCACTG   20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG   20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG   20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG   20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAG   20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC   20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG   20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATA ACCACCAGTG   20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACGGT GACAAGTGTG   20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC   20

            (2) INFORMATION FOR SEQ ID NO:103:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC   20

            (2) INFORMATION FOR SEQ ID NO:104:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG   20

            (2) INFORMATION FOR SEQ ID NO:105:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC   20

            (2) INFORMATION FOR SEQ ID NO:106:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG   20

            (2) INFORMATION FOR SEQ ID NO:107:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCAC   20

        (2) INFORMATION FOR SEQ ID NO:108:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 20 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTTGC AACCTGAGTG   20

        (2) INFORMATION FOR SEQ ID NO:109:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 20 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG   20

        (2) INFORMATION FOR SEQ ID NO:110:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 20 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG   20

        (2) INFORMATION FOR SEQ ID NO:111:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 20 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGTCTGTG   20

        (2) INFORMATION FOR SEQ ID NO:112:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 20 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC   20

        (2) INFORMATION FOR SEQ ID NO:113:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 20 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG   20

        (2) INFORMATION FOR SEQ ID NO:114:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG   20

        (2) INFORMATION FOR SEQ ID NO:115:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC   20

        (2) INFORMATION FOR SEQ ID NO:116:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC   20

        (2) INFORMATION FOR SEQ ID NO:117:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG   20

        (2) INFORMATION FOR SEQ ID NO:118:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCCAC   20

        (2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG   20

            (2) INFORMATION FOR SEQ ID NO:120:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC   20

            (2) INFORMATION FOR SEQ ID NO:121:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTTGAA GAAAGAGCTG   20

            (2) INFORMATION FOR SEQ ID NO:122:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG   20

            (2) INFORMATION FOR SEQ ID NO:123:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC   20

            (2) INFORMATION FOR SEQ ID NO:124:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTCACAGT CCCAAGGCTC   20

          (2) INFORMATION FOR SEQ ID NO:125:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGCGGTTGAG   20

          (2) INFORMATION FOR SEQ ID NO:126:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG   20

          (2) INFORMATION FOR SEQ ID NO:127:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG   20

          (2) INFORMATION FOR SEQ ID NO:128:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC   20

          (2) INFORMATION FOR SEQ ID NO:129:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG   20

          (2) INFORMATION FOR SEQ ID NO:130:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC   20

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG   20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG   20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGCAGTG   20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC   20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG   20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCAGTG GTGCCTGCAG   20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACGGT TGCCAACCTG   20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCTCTG   20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC   20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAGACTT CAACCTTCAC   20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 20 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC   20

            (2) INFORMATION FOR SEQ ID NO:142:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACC TTTACCTCAC   20

            (2) INFORMATION FOR SEQ ID NO:143:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAGATG   20

            (2) INFORMATION FOR SEQ ID NO:144:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTCAC   20

            (2) INFORMATION FOR SEQ ID NO:145:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG   20

            (2) INFORMATION FOR SEQ ID NO:146:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG   20

            (2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 4047 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

   (A) NAME/KEY: Coding Sequence
   (B) LOCATION: 378...1799
   (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
GGATCCAAAG GACGCCCCCG CCGACAGGAG AATTGGTTCC CGGGCCCGCG GCGATGCCCC      60
CCCGGTAGCT CGGGCCCGTG GTCGGGTGTT TGTGAGTGTT TCTATGTGGG AGAAGGAGGA     120
GGAGGAGGAA GAAGAAGCAA CGATTTGTCT TCTCGGCTGG TCTCCCCCCG GCTCTACATG     180
TTCCCCGCAC TGAGGAGACG GAAGAGGAGC CGTAGCCGCC CCCCTCCCG GCCCGGATTA      240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CCTTGGATTC AGACGCCGAT TCGCCCAGTG     300
TTTGGGAAAT GGGAAGTAAT GACAGCTGGC ACCTGAACTA AGTACTTTTA TAGGCAACAC     360
CATTCCAGAA ATTCAGG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT       410
                    Met Asn Gly Asp Met Pro His Val Pro Ile Thr
                     1               5                   10
```

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ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT      458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro
        15               20                   25
```

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CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT      506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn
        30                35                   40
```

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GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC      554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp
        45               50                   55
```

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AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT      602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp
60               65                70                   75
```

```
CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC      650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp
                 80                85                   90
```

```
ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC      698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe
             95                   100              105
```

```
AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG      746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met
            110                  115               120
```

```
TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT      794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser
        125              130               135
```

```
TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT      842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe
140              145               150                   155
```

```
GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT      890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn
                160                  165               170
```

```
AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG      938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met
            175                  180               185
```

```
CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA      986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln
            190                  195               200
```

```
GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT        1034
Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His
205                 210                 215

GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT        1082
Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His
220             225                 230                 235

GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG        1130
Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val
                240                 245                 250

CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT        1178
His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala
                255             260                 265

GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA        1226
Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly
            270             275             280

AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT        1274
Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser
285                 290                 295

CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG        1322
Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu
300                 305                 310                 315

CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA        1370
Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu
                320                 325                 330

GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA        1418
Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile
                335                 340                 345

ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT        1466
Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser
            350                 355                 360

CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT        1514
Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly
            365                 370                 375

GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG        1562
Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln
380                 385                 390                 395

TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC        1610
Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn
                400                 405                 410

CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA        1658
Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala
                415                 420                 425

TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT        1706
Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val
            430                 435                 440

GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT        1754
Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro
445                 450                 455

GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA     1804
Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
460                 465                 470

TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCCAGCT CTCTCCGTGA GCTCTGGGCC     1864
TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC     1924
CAGTTGGCTT CTCTCACTCG CTTCCTCCTG TGGAGAAGCC TGTCCAGGTG TCACTGCCTC     1984
CAGGAAGCTG TCTCTGATTT CTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT     2044
CGCTCTTGTC CCTGGAATTG TAACCATAGG TTTTCCTGTC TCCTGGAGGA CAAGGATGAG     2104
```

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```
GGCTTTCCAC TTGAGTCTCC CTGGTGGAGC CCAGCTCCTG ACATACCTGG TAAAAGTTCT   2164
CAAGAGAAGA ACATGGAGGA GGAATGTGGA TAACAACCCT GGCTGCCTGT GTGTTCCAAG   2224
CTAGGAAGAT GTAATGTCCC CACAAACGGG GTAAATGGCT TGCCTGCGTC ACAGCTGTCT   2284
CAAGCCCAGG CCCTGGGCGC CAGCCCAAGC CCAAGGACTA GGTCCAGAGC CACACAGCGC   2344
CAGGCCACAT CCGCCTCACC TGGGACCCTT TGTGGGGTAC AGTCTCCGGC CCCACCCAGA   2404
CCTCCTGAAG GAGAGACCCC ATGGCAAGGA CTCAGCCACC TGCAGTTTCA TAAGCCCCCA   2464
GTGGGTTCCT AGGCATGAAG ACCACCGGTT AGAGGCTGAA CTGGCAGGAA CCTGTCTCCA   2524
GCCCCTTCTC ACCCCAGCCG GGCCCTGCCT CAGAGGCAGC ACCCAGGACG TGGCCATGAC   2584
CCGTGGACTC CACTCAATCC CTCTTCTCCA GGAGCCATGC AAAGTGTCAG CCAGCCAGGC   2644
CCCTGGAAGG CAGTCATCAC CTCTTAAGGC ATTGTGGGTG TCGGTCCTGC AACTGCCAGG   2704
TGCAGCACAC GACCCGTGTC CGGTGTTCGA TAGCAGGGAG CCATGACCTG GCAACGATTC   2764
CACGCTCAAA GGGGCACCCG GGGGGCCCTG GGTCGGGGCG GATCAGCTTT CCCTGGGCAC   2824
ATCTGCCTCA TTCCAGATCT CCAGGGCTCA TGTCTGTGAC AGGGAGGGAA GGCTCTGCCC   2884
TGGCCTTCCG TCAGCTCTGC CAGTGCAGGC TGGGCAGCCT GGGCTTTAGA GCTGGCTTCT   2944
GCCCACACTT TCTCCGTGAA AGGAAAACAA CTATGAGTCT GCCAAACGCA TCTCAGATGC   3004
GTTTTAAAAA ATTCTGGTCC CCGCTCTCTG TCCCATCATC CGCCTCGGGG ACTTCCTCTC   3064
TCCGTGGTTC TCACCCCATA CTCTGTCACT GCCACATTTT CACCTGGGCC TGGCCTTTGT   3124
CTCCACCTGA AACTCCTGAA AATCTTGAAA TGGATTTCTA GGTCACTGGG GACTCCGGCA   3184
GCACATTCGG CTTCAGAATA AAGGGCGCCC GCGGTCCCCC AGCACCTCCC CAAGCCACAC   3244
CCCTAGCTTC CCTCCCTATC CCTGCAGCCT GAGGGTCCCT TCAGCCACCC TTAAGTCCCC   3304
ACCTGGGCTC CTGCCCCGCC CCTGGCTAGC AGCGCCTTCT CCACCGGGGC CCCCTCTGCT   3364
CACAGAGCCC CCTCACCTCC CTGGGGATGA GGGGCCAGGC CATGACCCTG AAAGTCTAGC   3424
CCTGGCCTTG ACCTCCCAGG AGCGCCCTCC CCGCCCTCTC CCGGCCCCGG CCCCGTCCTC   3484
TGCTGCTGGC CTCTGGGTCG TGCCCCGCAG ACTGAGCTGC GCTTGGGGGT CCTGGCGGCC   3544
TGGGCCGTCC CGCACCGAAC CCAGGCGGTC GGAGCCCGGC GGGAAGGCGC GAGGTCCTTC   3604
TGGGGGCTCC TCCGACGCCT GAGGGCGCTG CTTCCCCGCG GCCGCCCCGG GTTTCTGCGG   3664
AGCCGGGGCC TCCGCTCTCG GGTGACCCGG TGAGACCCCC GGGGAGGCCG CTGGGGAGGC   3724
GCGGGCTCTG CTCCCGGGTC CCAAACGCAC TGGCTGCCCC TCAGGAGGGA CGGCGACCTC   3784
CACCCACGGC GCTGGCGCCC GCACGGCCGC TCCTCCCGCT CCCGCAGCCT GGACGCCTCC   3844
CGAGGCCGCC CCGCCGGGCC CCACGCGCGG CCCCATCCGC AGGCCAGGAC TGCCTTCCCG   3904
GAGCTGGCGG CCCCCAGCCT GGAGGAGCCG GCCCCAGACG CCCTCCCAGC CCTCCCCAGC   3964
CCACTCTGGC CCCGCAGCCC CCGCCTGGTC CGAGTGCGGG TCTCTGGCCC CGGCCTTTCC   4024
CGGGGAAGGA AAGCAAAAAG CTT                                          4047
```

```
Met Asn Gly Asp Met Pro His Val Pro Ile Thr Thr Leu Ala Gly Ile
1             5                  10              15
Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro Leu Pro Ser Pro Leu
            20                  25              30
Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn Ala Arg Ile Ala Glu
            35                  40              45
Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp Asn Leu Val Ser Gln
50                  55                  60
Leu Val His Ser Leu Asn Gln Val Ser Thr Asp His Ile Glu Leu Lys
65                  70                  75              80
Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp Ile Pro Val Leu Leu
                85                  90              95
Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe Arg Glu Lys Ser Met
            100                 105             110
Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met Ser Gln Tyr Lys Leu
            115                 120             125
Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln
            130                 135             140
Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr
145                 150                 155             160
Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser
                165                 170             175
Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro
            180                 185             190
Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser
            195                 200             205
```

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```
Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
    210                 215             220
Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
225                 230             235                 240
His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser
                245             250                 255
Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
            260             265                 270
Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
        275             280             285
Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
    290             295             300
Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
305             310             315                 320
Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
            325             330                 335
Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
            340             345             350
Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
            355             360             365
Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
    370             375             380
Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
385             390             395                 400
Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
            405             410                 415
Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
            420             425                 430
Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
        435             440             445
Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
    450             455             460
Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
465                 470
```

(2) INFORMATION FOR SEQ ID NO:149:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 2998 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (ix) FEATURE:

       (A) NAME/KEY: Coding Sequence
       (B) LOCATION: 26...799
       (D) OTHER INFORMATION:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
AAGCTTTTTG AATTCGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG       52
                            Ala Thr Gln Ala Ile Phe Glu Ile Leu
                             1                   5

GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT      100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile
10                  15              20                  25

GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT      148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val
                30                  35                  40

ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA      196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln
                45                  50                  55

CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA      244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu
            60                  65                  70

GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA      292
```

```
        Gly Leu Gln Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val
           75                  80                  85

        GAG TTG CTT TTG AAA TCA GAA AGT CAG TGC AGG GTT GTA GTG TTG ATG        340
        Glu Leu Leu Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met
        90                  95                  100                 105

        GGC TCT ACT TCT GAT CTT GGT CAC TGT GAA AAA ATC AAG AAG GCC TGT        388
        Gly Ser Thr Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys
                        110                 115                 120

        GGA AAT TTT GGC ATT CCA TGT GAA CTT CGA GTA ACA TCT GCG CAT AAA        436
        Gly Asn Phe Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys
                    125                 130                 135

        GGA CCA GAT GAA ACT CTG AGG ATT AAA GCT GAG TAT GAA GGG GAT GGC        484
        Gly Pro Asp Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly
                    140                 145                 150

        ATT CCT ACT GTA TTT GTG GCA GTG GCA GGC AGA AGT AAT GGT TTG GGA        532
        Ile Pro Thr Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly
                    155                 160                 165

        CCA GTG ATG TCT GGG AAC ACT GCA TAT CCA GTT ATC AGC TGT CCT CCC        580
        Pro Val Met Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro
        170                 175                 180                 185

        CTC ACA CCA GAC TGG GGA GTT CAG GAT GTG TGG TCT TCT CTT CGA CTA        628
        Leu Thr Pro Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu
                        190                 195                 200

        CCC AGT GGT CTT GGC TGT TCA ACC GTA CTT TCT CCA GAA GGA TCA GCT        676
        Pro Ser Gly Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala
                        205                 210                 215

        CAA TTT GCT GCT CAG ATA TTT GGG TTA AGC AAC CAT TTG GTA TGG AGC        724
        Gln Phe Ala Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser
                        220                 225                 230

        AAA CTG CGA GCA AGC ATT TTG AAC ACA TGG ATT TCC TTG AAG CAG GCT        772
        Lys Leu Arg Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala
                        235                 240                 245

        GAC AAG AAA ATC AGA GAA TGT AAT TTA TAAGAAAGAA TGCCATTGAA TTTTTTA      826
        Asp Lys Lys Ile Arg Glu Cys Asn Leu
        250                 255

        GGGGAAAAAC TACAAATTTC TAATTTAGCT GAAGGAAAAT CAAGCAAGAT GAAAAGGTAA       886
        TTTTAAATTA GAGAACACAA ATAAAATGTA TTAGTGAATA AATGGTGAGG GTAGGCCTAT       946
        TCAGATGCAA GGCCAGCAAT GGGGCTCCCC ATTATCCCCA CCCCTTTGGT CCCAGTCCCC      1006
        TTCTCTGCAA TGGGCACGCA TAGAGGAGAG ACAAAGGGTA TTAGACGCAA CATCATTGGC      1066
        CCAGGGGAGT CCGAGAAGAG CTGCCATTGG CTGACAGGGC ATTTTCAGGC TCTGTCATTG      1126
        GTCAGGGAGC ACACCCCAGC CTGAAGAGTG ATGCCATTGG CCAGGGAGTG GTTTTGTCAT      1186
        AGCCGTTGGC TGTGAAGTGG AAGGAAAAGA TCTGGGAATG AAGCCCTGTG GCCAGGAAGA      1246
        TAGACAGGGC AGCAACTTCT GGGCCTCCAG GCCCTCTTCC CACCATAGCA ATGTGGGCAA      1306
        AACTGGTGTC AGGCCCCAGC CAGAAAAAGG AGCCCAAGCC AGAGGGCAAG TGACAAAGGA      1366
        TGTACCATGT CCAATCTCCC ACACCCTGGG GCTGCCCTTC CCAATGTCTT TCTTGATAGC      1426
        CAAGTTGGGC TGGGAGCAGC TCACTGCTCC TCTAGCCAGG AGGGTTTCTC AGCTCCTGGA      1486
        GGCCGCAGCT TGATGTTGAA CTGCTGCAGG GTCTGCTCCA GCTGTTTCTG GTTCCCAGCA      1546
        AAGTAGGCGG ACACGACCATT GTGGAAGAGC AGCAGCTGCT TGTGCATCAC CTTGATCTTG      1606
        TTTTCTTCCA GGAACTTGAG CTTGATGGCC ACATCTCCCC GCAGCTTCTC ATACTTGTCC      1666
        CGATGGGCCT GGAAAGTGGC CTGGGCACTC TCAAGTCGAC CACGTGTCCC TGCATCCCGG      1726
        GGGCCTAGAC TCAGCTCCTC TAAGTCTGTT CGGTAGGCAT CATATTCCAG CCTGGCAGCC      1786
        TCATACTGTT TCACAGTCAT GAGCGTGTCT TCCATGGTCT TGGTGACCAA TGTGTTGATG      1846
        CTAGAGACAA AGAAGTTCAC GGCTCCTAGC AGCGTTTCCC CATTCTTGCA TAGTAGTTTC      1906
        TGTGTCTCTG CATTGTAGCC AAATTCCTCC TGAAGCTCTG GGGACTTCTG GCTGAGGTCA      1966
        GCAAAGGCAT CACCCAGTGC ATGCTGGGTC TGCAGCAGGC TGTAGAGGTG GGCTGTCAGT      2026
        GCCCGGCCCA GCTGCAGGAC ACTCTCATAC TTGCGCTTCG TCTCACGCAG CAACTCAATC      2086
        TGCAGCTCTA GCTCCAGGAT TCCGGCGCCT CCACTCCGTC CCCCGCGGGT CTGCTCTGTG      2146
        TGCCATGGAC GGCATTGTCC CAGATATAGC CGTTGGTACA AAGCGGGGAT CTGACGAGCT      2206
        TTTCTCTACT TGTGTCACTA ACGGACCGTT TATCATGAGC AGCAACTCGG CTTCTGCAGC      2266
        AAACGGAAAT GACAGCAAGA AGTTCAAAGG TGACAGCCGA AGTGCAGGCG TCCCCTCTAG      2326
        AGTGATCCAC ATCCGGAAGC TCCCCATCGA CGTCACGGAG GGGGAAGTCA TCTCCCTGGG      2386
```

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```
GCTGCCCTTT GGGAAGGTCA CCAACCTCCT GATGCTGAAG GGGAAAAACC AGGCCTTCAT  2446
CGAGATGAAC ACGGAGGAGG CTGCCAATAC CATGGTGAAC TACTACACCT CGGTGACCCC  2506
TGTGCTGCGC GGCCAGCCCA TCTACATCCA GTTCTCCAAC CACAAGGAGC TGAAGACCGA  2566
CAGCTCTCCC AACCAGGCGC GGGCCCAGGC GGCCCTGCAG GCGGTGAACT CGGTCCAGTC  2626
GGGGAACCTG GCCTTGGCTG CCTCGGCGGC GGCCGTGGAT GCAGGGATGG CGATGGCCGG  2686
GCAGAGCCCC GTGCTCAGGA TCATCGTGGA GAACCTCTTC TACCCTGTGA CCCTGGATGT  2746
GCTGCACCAG ATTTTCTCCA AGTTCGGCAC AGTGTTGAAG ATCATCACCT TCACCAAGAA  2806
CAACCAGTTC CAGGCCCTGC TGCAGTATGC GGACCCCGTG AGCGCCCAGC ACGCCAAGCT  2866
GTCGCTGGAC GGGCAGAACA TCTACAACGC CTGCTGCACG CTGCCGCATCG ACTTTTCCAA  2926
GCTCACCAGC CTCAACGTCA AGTACAACAA TGACAAGAGC CGTGACTACC TCGTGCCGAA  2986
TTCTTTGGAT CC                                                       2998
```

(2) INFORMATION FOR SEQ ID NO:150:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 258 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (v) FRAGMENT TYPE: internal

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser Trp Leu Pro Gln
1               5                   10                  15
Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr
            20                  25                  30
Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg
        35                  40                  45
Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr
    50                  55                  60
Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys
65                  70                  75                  80
Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Leu Lys Ser Glu
                85                  90                  95
Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly
            100                 105                 110
His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys
        115                 120                 125
Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg
    130                 135                 140
Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala
145                 150                 155                 160
Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr
                165                 170                 175
Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val
            180                 185                 190
Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Gly Cys Ser
        195                 200                 205
Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe
    210                 215                 220
Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu
225                 230                 235                 240
Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys
                245                 250                 255
Asn Leu
```

    (2) INFORMATION FOR SEQ ID NO:151:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1038 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln
1               5                   10                  15
```

```
Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
             20                  25              30
Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
         35              40                  45
Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
     50                  55              60
Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
65              70                  75                      80
Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
             85                  90              95
Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
         100                 105                 110
Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Val Ser Asp
         115                 120                 125
Ser Ser Trp Gln Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
     130             135                 140
Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
145             150                 155                     160
Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
             165                 170                 175
Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
         180             185                 190
Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
         195                 200                 205
Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
     210             215                 220
Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
225             230                 235                     240
Arg Gln Gly Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
             245                 250                 255
Lys Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln
             260                 265                 270
Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
     275             280                 285
Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
     290             295                 300
Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
305             310                 315                     320
Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
             325                 330                 335
Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
         340                 345                 350
Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
         355                 360                 365
Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
     370             375                 380
Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu
385             390                 395                     400
Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
             405                 410                 415
Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
             420                 425                 430
Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
         435                 440                 445
Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
     450             455                 460
Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
465             470                 475                     480
Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
             485                 490                 495
Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
         500             505                 510
Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
         515             520                 525
Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
     530             535                 540
Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
545             550                 555                     560
Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
             565                 570                 575
Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
         580                 585                 590
Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg
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                595                600                605
Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys
    610            615                 620
Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr
625                 630                635                640
Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu
                645                650                655
Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro
                660                665                670
Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser
            675                680                685
Thr Ile Pro Ala Pro Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr
            690                695                700
Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val
705                 710                715                720
Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly
                725                730                735
Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala
                740                745                750
Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp
            755                760                765
Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr
    770                775                780
Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu
785                 790                795                800
Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu
                805                810                815
Asn Lys Leu Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu
                820                825                830
Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg
            835                840                845
Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu
    850                855                860
Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe
865                 870                875                880
Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu
                885                890                895
Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu
            900                905                910
Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu
    915                920                925
Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu
    930                935                940
Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln
945                 950                955                960
Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala
                965                970                975
Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp
            980                985                990
Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly
            995                1000                1005
Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg
    1010                1015                1020
Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Gln Lys Ala
1025                1030                1035
```

(2) INFORMATION FOR SEQ ID NO:152:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 849 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro
1               5               10                 15
Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro
            20                25                30
Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly
            35                40                45
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Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
50   55   60
Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
65   70   75   80
Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
        85   90   95
Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
        100   105   110
Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
    115   120   125
Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
    130   135   140
Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
145   150   155   160
Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
            165   170   175
Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
        180   185   190
Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
    195   200   205
Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
    210   215   220
Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
225   230   235   240
Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
            245   250   255
Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
        260   265   270
Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
    275   280   285
Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
290   295   300
Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
305   310   315   320
Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
            325   330   335
Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
        340   345   350
Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
    355   360   365
Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
    370   375   380
His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
385   390   395   400
Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
            405   410   415
Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
        420   425   430
Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
        435   440   445
Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
    450   455   460
Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
465   470   475   480
Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
            485   490   495
Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
        500   505   510
Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
    515   520   525
Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
    530   535   540
Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
545   550   555   560
Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
            565   570   575
Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
        580   585   590
Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
        595   600   605
Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
    610   615   620
Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

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625              630               635                 640
Val Tyr Met Ser Ile Cys Gly Glu Asn Glu Asn Cys Pro Pro Gly Val
                     645               650                655
Gly Ala Cys Phe Gly Gln Thr Arg Ile Ser Val Gly Lys Ala Asn Lys
             660               665               670
Arg Leu Arg Tyr Val Asp Gln Val Leu Gln Leu Val Tyr Lys Asp Gly
         675               680               685
Ser Pro Cys Pro Ser Lys Ser Gly Leu Ser Tyr Lys Ser Val Ile Ser
         690               695               700
Phe Val Cys Arg Pro Glu Ala Gly Pro Thr Asn Arg Pro Met Leu Ile
705               710               715               720
Ser Leu Asp Lys Gln Thr Cys Thr Leu Phe Phe Ser Trp His Thr Pro
             725               730               735
Leu Ala Cys Glu Gln Ala Thr Glu Cys Ser Val Arg Asn Gly Ser Ser
             740               745               750
Ile Val Asp Leu Ser Pro Leu Ile His Arg Thr Gly Gly Tyr Glu Ala
             755               760               765
Tyr Asp Glu Ser Glu Asp Asp Ala Ser Asp Thr Asn Pro Asp Phe Tyr
         770               775               780
Ile Asn Ile Cys Gln Pro Leu Asn Pro Met His Gly Val Pro Cys Pro
785               790               795               800
Ala Gly Ala Ala Val Cys Lys Val Pro Ile Asp Gly Pro Pro Ile Asp
             805               810               815
Ile Gly Arg Val Ala Gly Pro Pro Ile Leu Asn Pro Ile Ala Asn Glu
             820               825               830
Ile Tyr Leu Asn Phe Glu Ser Ser Thr Pro Cys Gln Glu Phe Ser Cys
             835               840               845
Lys


        (2) INFORMATION FOR SEQ ID NO:153:

            (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 852 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear


            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
1               5               10               15
Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
             20               25               30
Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
         35               40               45
Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
    50               55               60
Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys
65               70               75               80
His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
             85               90               95
Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
             100               105               110
Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
         115               120               125
Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
    130               135               140
Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
145               150               155               160
Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
                 165               170               175
Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
         180               185               190
Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser
         195               200               205
Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
    210               215               220
Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
225               230               235               240
Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
                 245               250               255
```

Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
         260   265   270

Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
      275   280   285

Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
      290   295   300

Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
305   310   315   320

Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
         325   330   335

Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
         340   345   350

His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
         355   360   365

Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro
      370   375   380

Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
385   390   395   400

Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
         405   410   415

Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
         420   425   430

Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
         435   440   445

Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
         450   455   460

Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
      465   470   475   480

Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
         485   490   495

Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
         500   505   510

Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
         515   520   525

Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
         530   535   540

Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
545   550   555   560

Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
         565   570   575

Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
         580   585   590

Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Glu Trp Gly Leu Ala Arg His
         595   600   605

Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
      610   615   620

Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
625   630   635   640

Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
         645   650   655

Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
         660   665   670

Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
         675   680   685

Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
         690   695   700

Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
705   710   715   720

Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
         725   730   735

Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
         740   745   750

Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
         755   760   765

Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
         770   775   780

Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
785   790   795   800

Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile
         805   810   815

Gln Leu Gly Glu Asp Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn
         820   825   830

Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

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Leu Lys Glu Asp
      850

      (2) INFORMATION FOR SEQ ID NO:154:

         (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 693 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Phe Ser Ala Leu Lys Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
1   5   10   15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
            20   25   30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
        35   40   45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
    50   55   60
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
65   70   75   80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
                85   90   95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
            100   105   110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala
        115   120   125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
    130   135   140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145   150   155   160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
                165   170   175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg
            180   185   190
Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg
        195   200   205
Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His
    210   215   220
Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu
225   230   235   240
Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu
                245   250   255
Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu
                260   265   270
Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala
            275   280   285
Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala
    290   295   300
Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala
305   310   315   320
Pro Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val
                325   330   335
Pro Pro Ser Glu Ala Leu Pro Pro Pro Ala Cys Pro Ser Ala Pro Ala
            340   345   350
Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr
        355   360   365
Glu Ala Ala Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro
    370   375   380
Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp
385   390   395   400
Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val
                405   410   415
Gly Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu
            420   425   430
Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu
        435   440   445
Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser
    450   455   460

```
Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
465             470             475             480
Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
            485             490             495
Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
            500             505             510
Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr
        515             520             525
Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
        530             535             540
Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
545             550             555             560
Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
            565             570             575
Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
            580             585             590
Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
        595             600             605
Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
    610             615             620
Ser Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser
625             630             635             640
Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
            645             650             655
Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
            660             665             670
Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
        675             680             685
Tyr Ser Glu Ser Tyr
    690
```